pre-S gene was mutated in 72% of the patients. Deletions across pre-S1/pre-S2, pre-S2 initiation codon mutations with internal deletions and S gene nonsense mutations were prevalent. The HBV mutations described in this study have been associated with increased risk for HCC.

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67.025

Seroprevalence of Human Immunodeficiency Virus, Hepatitis B and C Viruses Among Blood Donors in Chabahar Iran

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Background: Transfusions can be a quick and easy route for the transmission of infectious agents such as HIV, HBV and HCV. Evaluation of the prevalence among blood donors (BDs) is a common and easy method to obtain the epidemiology of these infections in a community. We performed this study to determine HIV, HBV and HCV seroprevalence among BDs in one of the main commercial ports in Iran.

Methods: The sample included 5409 consecutive donors (17—65 years) who donated blood from 2002 to 2003. HBsAg, anti-HCV and anti-HIV were investigated by ELISA in blood samples. If the results of ELISA samples were reported to be positive in the HIV and HCV cases, the confirmation was done with RIBA/Western blot

Results: Most of BDs were motivated ones with 42%; who donate at regular intervals, 38% were first-time voluntary and 20% were voluntary donors with the history of at least one donation. Among BDs, 95.7% were male. The seroprevalence of HBsAg, HCV-Ab and HIV-Ab among BDs was 2.4%, 3.7% and 1.3% respectively in the first evaluation while 78.1% of positive HCV-Ab and 92.3% of positive HIV-Ab were negative in RIBA (Western blot). The prevalence of HBsAg and HCV infections among first BDs differ from other donors significantly. Also married persons were infected with HBV and HCV more than singles.

Conclusion: HIV and hepatitis transmission through blood transfusion is a major concern in developing countries such as Iran where economic constraints limit blood supply safety. On the other hand, demand for blood transfusion is high and despite tremendous strides in preventing viral infection through careful donor screening and viral testing, it is remain the risk transfusion-transmissible viral diseases.

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Phylogenetic Analysis of a Hepatitis C Virus Nosocomial Outbreak

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Background: Chronic viral hepatitides, their long-term consequences, the great number of individuals passed through infection and socio-economic implications represent arguments for comprehensive studying of these diseases. Hepatitis C virus (HCV) infection is endemic all over the world, its prevalence varying between 0.5% and 5%. HCV genotype and viral load affect treatment response. HCV genome is conserved among genotypes but the variability of the virus variants allows tracing infections by sequence analysis. In order to evaluate the nosocomial transmission of HCV infection in a urology clinic, a phylogenetic analysis of HCV strains was performed in the core genomic region.

Methods: Using COBAS CORE II ELISA technique for detecting anti-HCV antibodies we tested ten sera prelevated from a urology clinic. We performed COBAS AMPLICOR HCV MONITORTM test in the positive sera for the viral load. We found a significant viral load in seven cases, which were submitted to Neighbor-Joining phylogenetic analysis and interpreted with MEGA 3 Program. The phylogenetic analysis, based on the HCV core region, was realized by comparing the amplified sequences from the four sera with other Romanian sequences from genotype 1b strains and with other different geographic genotypes' sequences, selected from data bases

Results: We found a strong recent epidemiological link for three genotype 1b strains, which form a group, the genetic distance between them being very short (0.004—0.007). The other HCV strains served as controls and manifested different lineage degrees between themselves or compared with other analyzed strains.

Conclusion: This study confirmed the strong relationship between three HCV strains and the nosocomial transmission of the infection. Phylogenetic analysis in the core region represents a useful tool for tracing infections and routes of viral transmission.

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Molecular Epidemiology of HCV Genotypes in Injecting Drug Users in Hong Kong

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Background: Previous studies have shown that both genotypes 1b and 6a HCV were common among injecting drug users (IDU) in Hong Kong, but absence of subjects characteristics make further understanding of the molecular epidemiology difficult. We earlier reported a high prevalence of 85% of HCV in local IDUs. The present analysis was subsequently conducted to characterize the HCV genotypes